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RAW SEQUENCE LISTING PATENT APPLICATION US/09/040,485

TEAM 1

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	This Raw Listing contains the General Information Section and up to the first 5 pages.
1 2	SEQUENCE LISTING SEQUENCE LISTING
3 4	(1) General Information:
5 6	(i) APPLICANT: Radosevich, James A.
7 8 9	(ii) TITLE OF INVENTION: A GENE ENCODING A NOVEL MARKER FOR CANCER
10 11	(iii) NUMBER OF SEQUENCES: 9
12 13 14 15 16 17 18	<pre>(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: BRINKS, HOFER, GILSON & LIONE (B) STREET: NBC Tower - Suite 3600, 455 N. Cityfront</pre>
20 21 22 23 24 25 26	 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 28 29 30 31	(vi) CURRENT APPLICATION DATA:(A) APPLICATION NUMBER: US 09/040,485(B) FILING DATE: 17-MAR-1998(C) CLASSIFICATION:
32 33 34 35 36	<pre>(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Martin, Alice O. (B) REGISTRATION NUMBER: 35,601 (C) REFERENCE/DOCKET NUMBER: 8998/3</pre>
37 38 39 40 41	(ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 312-321-4200 (B) TELEFAX: 312-321-4299
42 43	(2) INFORMATION FOR SEQ ID NO:1:
44 45 46	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 2442 base pairs(B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/09/040,485

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62	ACG'	rggt'				TT G											108
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82	GTG	GAG	GCA	GAA	CCC	CAG	ΔΑΤ	АТС	GAA	GAT	GAA	GCA	ΔΑΔ	GAA	CAA	Δጥጥ	348
83						Gln											
84			80					85					90				
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86	CAG	TCC	CTT	CTC	CAT	GAA	ATG	GTA	CAC	GCA	GAA	CAT	GTT	GAG	GGA	GAA	396
87	Gln	Ser	Leu	Leu	His	Glu	Met	Val	His	Ala	Glu	His	Val	Glu	Gly	Glu	
88		95					100					105			-		
89																	
90	GAC	TTG	CAA	CAA	GAA	GAT	GGA	CCC	ACA	GGA	GAA	CCA	CAA	CAA	GAG	GAT	444
91						Asp											
92	110					115	-			-	120					125	
93																	
94	GAT	GAG	TTT	CTT	ATG	GCG	ACT	GAT	GTA	GAT	GAT	AGA	TTT	GAG	ACC	CTG	492
95	Asp	Glu	Phe	Leu	Met	Ala	Thr	Asp	Val	Asp	Asp	Arg	Phe	Glu	Thr	Leu	
96					130					135					140		
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98						CAT											540
99	Glu	Pro	Glu	Val	Ser	His	Glu	Glu	Thr	Glu	His	Ser	Tyr	His	Val	Glu	

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101	200	
102	GAG ACA GTT TCA CAA GAC TGT AAT CAG GAT ATG GAA GAG ATG ATG TCT	588
103	Glu Thr Val Ser Gln Asp Cys Asn Gln Asp Met Glu Glu Met Met Ser	
104	160 165 170	
105		
106	· · · · · · · · · · · · · · · · · · ·	636
107	Glu Glu Asn Pro Asp Ser Ser Glu Pro Val Val Glu Asp Glu Arg	
108 109	175 180 185	
110	TTG CAC CAT GAT ACA GAT GAT GTA ACA TAC CAA GTC TAT GAG GAA CAA	684
111	Leu His His Asp Thr Asp Asp Val Thr Tyr Gln Val Tyr Glu Glu Gln	004
112	190 195 200 205	
113		
114	GCA GTA TAT GAA CCT CTA GAA AAT GAA GGG ATA GAA ATC ACA GAA GTA	732
115	Ala Val Tyr Glu Pro Leu Glu Asn Glu Gly Ile Glu Ile Thr Glu Val	
116	210 215 220	
117		
118		780
119	Thr Ala Pro Pro Glu Asp Asn Pro Val Glu Asp Ser Gln Val Ile Val	
120	225 230 235	
121 122	GAA GAA GTA AGC ATT TTT CCT GTG GAA GAA CAG CAG GAA GTA CCA CCA	828
123	Glu Glu Val Ser Ile Phe Pro Val Glu Glu Gln Gln Glu Val Pro Pro	020
124	240 245 250	
125	240 243 250	
126	GAT ACT TAAAGCTTCA AAAAGACTGC CCCTACCACC ACAGGAGGAC CAGCCTAACC	884
127	Asp Thr	
128	255	
129		
130	ATACGCTCCA AAAGATGGCT GTGATAGATC TTGTGAAGCA ATTACTGAGC AGATCAAGAT	944
131		
132	CTTTGGGAAG GAACACTAAA GATGTTTTGA ATGAATTATA GTCCACTGGC ATTTTAGTGT 1	004
133	AMMONOMENT COMMONOMICAL ACACACAMON CONTAINING CANCER CANCERS AND MCCOCCAMON	064
134 135	ATTTTTTTT CTTTTTAGAA ACACACATTT CTAAAAATGT CATGTTACAT TCCTGCATGT 1	064
136	CCCTTTTGAT AGCATTAGTG GATCCATTGG ATTTCTTTTT TCTTTTTGTG AGACAGCTTT 1	124
137	coordinate descention will continue abacade in	124
138	TAGTCTTACC TGAATTTATG TGTGTTTTTC CGACAGTGGT TAATAATTAT ATTGGTGATG 1	184
139		
140	TAGCAGCAAT TGTGTTGGCA GGGTTTTCAT ATATTATTAG TAATTAACAC TAACTGTTGG 1	244
140 141		
140 141 142		244 304
140 141 142 143	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1	304
140 141 142 143 144	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1	
140 141 142 143 144 145	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1	304 364
140 141 142 143 144 145	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1	304
140 141 142 143 144 145 146	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1 CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTCAG ATTAACACTT 1	304 364 424
140 141 142 143 144 145 146 147	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1 CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTCAG ATTAACACTT 1	304 364
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140 141 142 143 144 145 146 147 148	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1 CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTCAG ATTAACACTT 1 TTGAAACCTT TGTAGCTTTT AGCTGATTAA TTAGAAAAAAT TAATATTTCA GTGAAAGTTT 1	304 364 424
140 141 142 143 144 145 146 147 148 149	ACTGACTTGT GTACACTGTG TTAAACATGA TTTAAAAGCT ATTAAGAGTA CTTTGTGTTA 1 GCACTCTTAA AAACGCTAAC AGAGATCATC ATTAGCTGTG AAGATTTGAG TTGTATATAC 1 CTGCACTGAT ATTCTTATCA AAAATTTCTA CATTAGCTTT AAGTGTTCAG ATTAACACTT 1 TTGAAACCTT TGTAGCTTTT AGCTGATTAA TTAGAAAAAAT TAATATTTCA GTGAAAGTTT 1 TAAAATTATCA TTTATTTATT TTTTTAAATG AGAGGGGAAA GCTGAAATTC CTTGTTAAGA 1	304 364 424 484

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153 154	TTA	ATCAT	TAT	AATA	GCTA'	га с	TCTC	TTCAC	G CA	TTTG'	ттта	AAT'	гтта	GAA	AACC'	TGTAT.	A 1664
155																	
156	AATT	CACTO	3GT	GCAT	AACT'	ra a	AGAT'	TATTO	TG	CCTT'	TGGC	TAA	TTGA(GTA	ATTC	C 1724	
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176	ATA	ATAA <i>I</i>	AAC	TCTT	CATT	rt G	'TGAA'	TAT	A GA	AGCT.	ACTT	TTT	ATAA	AGC	CATA	ידדדדי	T 2324
177																	
178 179	TAGO	3GAA <i>F</i>	ACT	AAGG	AGTG	AC A	TAGA	AC'I'G <i>I</i>	A TG.	AA'I'G	AGTA	AAA	3TAA0	GTT	TTGC'	rggat'	T 2384
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183	(2)	INFO	ORMA	TION	FOR	SEQ	ID I	NO:2	:								
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185	(i) SEQUENCE CHARACTERISTICS:																
186 187	(A) LENGTH: 255 amino acids																
188	(B) TYPE: amino acid (D) TOPOLOGY: linear																
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213				100					103					110			
215	G1 n	Glu	Δsn	Glv	Pro	Thr	G1 v	Glu	Pro	Gln	Gln	Glu	Asn	Δsn	Glu	Pho	
216	0111	GIG	115	GLY	110	1111	СТУ	120	FIO	GIII	GIII	GIU	125	АЗР	GIU	riie	
217													123				
218	Leu	Met	Ala	Thr	Asp	Val	Asp	Asp	Ara	Phe	Glu	Thr	Leu	Glu	Pro	Glu	
219		130					135		5			140					
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221	Val	Ser	His	Glu	Glu	Thr	Glu	His	Ser	Tyr	His	Val	Glu	Glu	Thr	Val	
222	145					150				-	155					160	
223																	
224	Ser	Gln	Asp	Cys	Asn	Gln	Asp	Met	Glu	Glu	Met	Met	Ser	Glu	Gln	Glu	
225					165					170					175		
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227	Asn	Pro	Asp		Ser	Glu	Pro	Val		Glu	Asp	Glu	Arg		His	His	
228			*	180					185					190			•
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230	Asp	Thr	_	Asp	Val	Thr	Tyr		Val	Tyr	Glu	Glu		Ala	Val	Tyr	
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238																	
239	Ser	Ile	Phe	Pro	Val	Glu	Glu	Gln	Gln	Glu	Val	Pro	Pro	Asp	Thr		
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